

P#19

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/555,981C

DATE: 04/23/2002 P.8
TIME: 07:57:28

Input Set : A:\5008.ST25.txt
Output Set: N:\CRF3\04232002\I555981C.raw

3 <110> APPLICANT: Lead B.V.
4 NOTEBORN, Mathieu Hubertus Maria
5 DAMEN-VAN OORSCHOT, Astrid Adriana Anna Maria
7 <120> TITLE OF INVENTION: MOLECULES INTERACTING WITH APOPTIN
9 <130> FILE REFERENCE: 2906-5008
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/555,981C
12 <141> CURRENT FILING DATE: 2000-06-26
14 <160> NUMBER OF SEQ ID NOS: 16
16 <170> SOFTWARE: PatentIn version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 17
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <221> NAME/KEY: misc_feature
25 <223> OTHER INFORMATION: Description of Artificial Sequence: pACT-specific sequenceing
prim
26 e
29 <400> SEQUENCE: 1
30 taccactaca atggatg
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 15
35 <212> TYPE: PRT
36 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <221> NAME/KEY: misc_feature
40 <223> OTHER INFORMATION: Description of Artificial Sequence; Hou/Nmi-like protein
putative
41 immunogenic peptid
44 <400> SEQUENCE: 2
46 Arg Asn Gly Gly Gly Glu Val Asp Arg Val Asp Tyr Asp Arg Gln
47 1 5 10 15
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 16
51 <212> TYPE: PRT
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <221> NAME/KEY: misc_feature
56 <223> OTHER INFORMATION: Description of Artificial Sequence: IEP35-like protein
putative i
57 immunogenic peptid
60 <400> SEQUENCE: 3
62 Cys Gln Leu Arg Lys Glu Leu Gly Asp Ser Pro Lys Asp Lys Val Pro
63 1 5 10 15

65 <210> SEQ ID NO: 4
66 <211> LENGTH: 658

RAW SEQUENCE LISTING
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Input Set : A:\5008.ST25.txt
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67 <212> TYPE: DNA
68 <213> ORGANISM: Homo sapien
70 <220> FEATURE:
71 <221> NAME/KEY: misc_feature
72 <223> OTHER INFORMATION: N is an undefined base
75 <400> SEQUENCE: 4
76 gggggatcat ggaagctgat aaagatgaca cacaacaaat tcttaaggag cattcgccag      60
78 atgaatttat aaaagatgaa caaaataagg gactaattga tgaaattaca aagaaaaata      120
80 ttcaactaaa gaaggagatc caaaagctt aaacggagtt acaagaggct accaaagaat      180
82 tccagattaa agaggatatt cctgaaacaa agatgaaatt ctatcgtt gaaactcctg      240
84 agaatgacag ccagttgtca aatatctcct ttcgttca agtgagctcg aaagtccctt      300
86 atgagataca aaaaggacaa gcacttacat cctttaaaaa agaagaagtt gctaaaaatg      360
88 tggtaagcat gagtaaacat catgtacaga taaaagatgt aaatctggag gttacggcca      420
90 agccagttcc attaaattca ggagtcatat tccaggttta ttagaaagtt tctaaaatga      480
92 aaatcaatgt tactgaaatt cctgacatcat tgcgtgaaga tcaaattgaga gacaaactag      540
W--> 94 agctgagctt ttcaaagtcc cggaaatggga ggcggagang tggaccgcgt gggactatga      600
W--> 96 cagacagtcc gggagtgcatat tcatcacgtt tggnggagat tggagtgcc tgacannn      658
99 <210> SEQ ID NO: 5
100 <211> LENGTH: 719
101 <212> TYPE: DNA
102 <213> ORGANISM: Homo sapien
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <223> OTHER INFORMATION: N is an undefined base
109 <400> SEQUENCE: 5
110 cggagttaca agaggctacc aaagaattcc agattaaaga ggatattcct gaaacaaaaga      60
W--> 112 tggaaattctt atcaggatgaa actcctgana atgacagccca gttgtcaat atctcctgtt      120
114 cggttcaagg tgagctcgaa agttcctttag gagataaaaaa aaggacaatg cacttacac      180
W--> 116 ctttggaaaaa ggaagaagtt gctaaaaatg tgnntaangc atgagtaaac atcatgtaca      240
118 gataataaga tgtaaatctg gaggttacgg ccaaagccaa gttccattaa tattcaagga      300
W--> 120 gtcangattc cagnntttat gctagaangt ttctaaaaat ganaatcaat gttactgga      360
W--> 122 aattccctgga cacatcgcn tggaaagatca agatgacgaa gacaaactaa gaagctgagc      420
W--> 124 ttttccaaag tcccggaaaana tggaaagagcg gtagagggtg gnaccgcgtg nganctatga      480
W--> 126 caagacaagn cggggaaagn tgcagtccat cacgttgcgtt nagaattgg angtnggctg      540
W--> 128 accaangaat ttggaaaaag gagangaatt accccctctt angagtaana tcaaaaccct      600
W--> 130 gccataanaa gtnactggt ttcnccatt acacagnant tacannttga ncaanantan      660
W--> 132 ncaggataat ttncaggggaa anaatctnaa gnatggcaag ntgacttctg gacaanggt      719
135 <210> SEQ ID NO: 6
136 <211> LENGTH: 220
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 6
142 His Glu Gly Arg Gly Ile Met Glu Ala Asp Lys Asp Asp Thr Gln Gln
143 1           5           10          15
145 Ile Leu Lys Glu His Ser Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn
146 20          25          30
148 Lys Gly Leu Ile Asp Glu Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys
149 35          40          45
151 Glu Ile Gln Lys Leu Glu Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe

```

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```

152      50          55          60
154 Gln Ile Lys Glu Asp Ile Pro Glu Thr Lys Met Lys Phe Leu Ser Val
155 65           70           75           80
157 Glu Thr Pro Glu Asn Asp Ser Gln Leu Ser Asp Ile Ser Cys Ser Phe
158           85           90           95
160 Gln Val Ser Ser Lys Val Pro Thr Glu Ile Gln Lys Gly Gln Ala Leu
161           100          105          110
163 Ile Thr Phe Glu Lys Glu Glu Val Ala Gln Asn Val Val Ser Met Ser
164           115          120          125
166 Lys His His Val Gln Ile Lys Asp Val Asn Leu Glu Val Thr Ala Lys
167           130          135          140
169 Pro Val Pro Leu Asn Ser Gly Val Arg Phe Gln Val Thr Val Glu Val
170 145           150          155          160
172 Ser Lys Met Lys Ile Asn Val Thr Glu Ile Pro Asp Thr Leu Arg Glu
173           165          170          175
175 Asp Gln Met Arg Arg Lys Leu Glu Leu Ser Phe Ser Lys Ser Arg Asn
176           180          185          190
178 Gly Arg Arg Arg Cys Gly Pro Arg Gly Thr Met Thr Asp Ser Pro Gly
179           195          200          205
181 Val Gln Ser Ser Arg Leu Val Glu Ile Gly Ser Gly
182           210          215          220
184 <210> SEQ ID NO: 7
185 <211> LENGTH: 307
186 <212> TYPE: PRT
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 7
191 Met Glu Ala Asp Lys Asp Asp Thr Gln Gln Ile Leu Lys Glu His Ser
192 1           5           10          15
194 Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn Lys Gly Leu Ile Asp Glu
195           20           25           30
197 Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys Glu Ile Gln Lys Leu Glu
198           35           40           45
200 Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe Gln Ile Lys Glu Asp Ile
201           50           55           60
203 Pro Glu Thr Lys Met Lys Phe Leu Ser Val Glu Thr Pro Glu Asn Asp
204 65           70           75           80
206 Ser Gln Leu Ser Asn Ile Ser Cys Ser Phe Gln Val Ser Ser Lys Val
207           85           90           95
209 Pro Tyr Glu Ile Gln Lys Gly Gln Ala Leu Ile Thr Phe Glu Lys Glu
210           100          105          110
212 Glu Val Ala Gln Asn Val Val Ser Met Ser Lys His His Val Gln Ile
213           115          120          125
215 Lys Asp Val Asn Leu Glu Val Thr Ala Lys Pro Val Pro Leu Asn Ser
216 130           135          140
218 Gly Val Arg Phe Gln Val Thr Val Glu Val Ser Lys Met Lys Ile Asn
219 145           150          155          160
221 Val Thr Glu Ile Pro Asp Thr Leu Lys Glu Asp Gln Met Arg Asp Lys
222           165          170          175
224 Leu Glu Leu Ser Phe Ser Lys Phe Arg Asn Gly Gly Glu Val Asp

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225	180	185	190
227	Arg Val Asp Tyr Asp Arg Gln Ser Gly Ser Ala Val Ile Thr Phe Val		
228	195	200	205
230	Glu Ile Gly Val Ala Asp Lys Ile Leu Lys Lys Glu Tyr Pro Leu		
231	210	215	220
233	Tyr Ile Asn Gln Thr Cys His Arg Val Thr Val Ser Pro Tyr Thr Glu		
234	225	230	235
236	Ile His Leu Lys Lys Tyr Gln Ile Phe Ser Gly Thr Ser Lys Arg Thr		240
237	245	250	255
239	Val Leu Leu Thr Gly Met Glu Gly Ile Gln Met Asp Glu Glu Ile Val		
240	260	265	270
242	Glu Asp Leu Ile Asn Ile His Phe Gln Arg Ala Lys Asn Gly Gly Gly		
243	275	280	285
245	Glu Val Asp Val Val Lys Cys Ser Leu Gly Gln Pro His Ile Ala Tyr		
246	290	295	300
248	Phe Glu Glu		
249	305		
251	<210> SEQ ID NO: 8		
252	<211> LENGTH: 659		
253	<212> TYPE: DNA		
254	<213> ORGANISM: Homo sapiens		
256	<220> FEATURE:		
257	<221> NAME/KEY: misc_feature		
258	<223> OTHER INFORMATION: N is an undefined base		
261	<400> SEQUENCE: 8		
262	agcagggtct gcaacaaaag gagcacacga tcaacatgga ggagtgcggg ctgcgggtgc	60	
264	aggccatccc cttggagctg cccatggtca ccaccatcca ggtgtccagc cagttgagtg	120	
266	gccggaggg gttgtcaact ggatttcctg ccagcctcag gctgagttag gagggagctgc	180	
W-->	268 tggacaanct anagatcttc tttggcaaga ctagaaacgg aggtggcnat gtggacnttc	240	
W-->	270 ggganctact gccagggant gtcatgctgg ggtttgctag ggatggatg gctcancgtc	300	
W-->	272 tgtgccaaatt cggccatttc acagtgccac tgggtggca gcangtcct ctgagagtct	360	
W-->	274 ctccgtatgt gaatggggan atccagangg ctganatcag gtcncagcca nttccccgt	420	
276	cggtaacttgt gtcacacatt cctgataatct tggatggccc ggagctgcat gacgtcctgg	480	
W-->	278 anatccactt ccagaanccc acccgcgaaaa gcgaggatgt aagacgcct gacagtcgta	540	
W-->	280 ccccaaggac aacagggcct aacagtcttc acctcctgaa tcaaggctan gggccctcccc	600	
W-->	282 cttctcatcc tcccccccccc cccgc当地 aactggccctg ggcttntg	659	
285	<210> SEQ ID NO: 9		
286	<211> LENGTH: 630		
287	<212> TYPE: DNA		
288	<213> ORGANISM: Homo sapiens		
290	<220> FEATURE:		
291	<221> NAME/KEY: misc_feature		
292	<223> OTHER INFORMATION: N is an undefined base		
295	<400> SEQUENCE: 9		
296	ccaaagtggc tgaggcagggt ctgcaacaaa aggacacac gatcaacatg gaggagtgcc	60	
298	ggctgcgggt gcagggtccag cccttggagc tgcccatggt caccaccatc cagggttcca	120	
300	gccagggttag tggccggagg gtgttggtca ctggatttcc tgccagcctc aggctgatgt	180	
302	aggaggagct gtcggacaag ctagatgtct tcttggcaa gacttaggaac ggagggtggcg	240	
304	atgtggacgt tcgggagcta ctgcccaggaa gtgtcatgct ggggtttgtt agggatggag	300	

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W--> 306	tggctcagcg	tctgtccaa	atcggccaag	ttcacagtgc	cactgggtgg	gcancaagtc	360									
W--> 308	cctctgagag	tcttcccgt	ta t g a t g g g	g a g a t c c a g a	a g g c t g a g a t	c a g g t c g c a n	420									
W--> 310	ccagttcccc	n c t c g t a c t	g g g t g c t c a a	c a t t c c t g a t	a t c t t g g a t t	g g c c c g g a g c	480									
W--> 312	tgc a t n a c g t	c c t g g a n a t c	a a c t t c a n a a	g c c c a c c c g c	c g g g g c n g n g	a g g t a n a a g g	540									
W--> 314	c c t g a c a t c n	t t a c c c a a a	g g a c a g c a t g	g n c c t a a c a g	t c c t c a c c t c	c n a a t c a n g c	600									
W--> 316	t n n g g g c t n	c c c t t c t a n c	n t c c c a a c t g				630									
319 <210>	SEQ ID NO:	10														
320 <211>	LENGTH:	631														
321 <212>	TYPE:	DNA														
322 <213>	ORGANISM:	Homo sapiens														
324 <220>	FEATURE:															
325 <221>	NAME/KEY:	misc_feature														
326 <223>	OTHER INFORMATION:	N is an undefined base														
329 <400>	SEQUENCE:	10														
330	g g a t c c a c t g	c c c t c t g c t t	g c g g g c t c t g	c t c t g a t c a c	c t t t g a t g a c	c c c a a a g t g g	60									
332	c t g a g c a g g t	g c t g c a a c a a	a a g g a g c a c a	c g a t c a a c a t	g g a g g a g t g c	c g g c t g c g g g	120									
334	t g c a g g t c c a	g c c c t t g g a g	c t g c c c a t q	t c a c c a c c a t	c c a g g t g a t g	g t g t c c a g c c	180									
W--> 336	a n t t g a g t g g	c c g g a g g g t g	t t g g t c a c t g	g a t t t c c t g c	c a g c c t c a g g	c t g a n t g a g g	240									
W--> 338	a g g a g c t g c t	g g a c a a g c t a	t g a g a t c t c	t t t g g c a a n a	c t a n g a a c g g	a n g t g g c g a t	300									
340	g t g g a c g t t c	g g g a g c t a c t	g c c a g g g a g t	g t c a t g c t g g	g g t t t g c t a c	g g a t g g a g t g	360									
342	g o t c a g c g t c	t g t g c c a a a t	c g g c c a g t t c	a c a a g t g c c a	c t g g g t g g g c	a g c a a g t c c c	420									
W--> 344	t c t g a g a g t c	t c t c c g t a t g	t g a n t g g n g a	g a t c a g a a t g	c t g a n a t t a a	g t c g c a t c c a	480									
W--> 346	a t t c c t c g c t	c n g g t a c t g g	t g t c a n n a t	c c t g a n a t c t	t g g a t t g g c c	c c n g a n t n c a	540									
W--> 348	t g a n a t c t g g	n a g a t t c a a t	t n c a n a a g t c	c a n c c n n c n g	n g n c g g a a g	t a n a g c c c g	600									
W--> 350	a n a n t t c n t n	n c n t a n g g n c	a g c a n n g c t	g			631									
353 <210>	SEQ ID NO:	11														
354 <211>	LENGTH:	138														
355 <212>	TYPE:	PRT														
356 <213>	ORGANISM:	Homo sapiens														
358 <400>	SEQUENCE:	11														
360	H i s	G l u	G l y	P r o	L y s	V a l	A l a	G l u	G l n	G l n	L y s	G l u	H i s			
361	1				5			10				15				
363	T h r	I l e	A s n	M e t	G l u	G l u	C y s	A r g	L e u	A r g	V a l	G l n	V a l	P r o	L e u	
364						20			25			30				
366	G l u	L e u	P r o	M e t	V a l	T h r	T h r	I l e	G l n	V a l	S e r	S e r	G l n	L e u	S e r	G l y
367						35			40			45				
369	A r g	A r g	V a l	L e u	V a l	T h r	G l y	P h e	P r o	A l a	S e r	L e u	A r g	L e u	S e r	G l u
370						50			55			60				
372	G l u	G l u	L e u	L e u	A s p	L y s	L e u	G l u	I l e	P h e	P h e	G l y	L y s	T h r	A r g	A s n
373						65			70			75			80	
375	G l y	G l y	G l y	A s p	V a l	A s p	V a l	A r g	G l u	L e u	L e u	P r o	G l y	S e r	V a l	M e t
376						85			90			95				
378	L e u	G l y	P h e	A l a	A r g	A s p	G l y	V a l	A l a	G l n	A r g	L e u	C y s	G l n	I l e	G l y
379						100			105			110				
381	G l n	V a l	H i s	S e r	A l a	T h r	G l y	T r p	A l a	S e r	S e r	P r o	S e r	G l u	S e r	L e u
382						115			120			125				
384	S e r	V a l	C y s	G l u	T r p	G l y	A s p	P r o	G l u	G l y						
385						130			135							
387 <210>	SEQ ID NO:	12														

VARIABLE LOCATION SUMMARY
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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:4; N Pos. 579,634,656,657,658
Seq#:5; N Pos. 89,213,218,305,314,328,343,380,439,462,471,474,490,500,520
Seq#:5; N Pos. 521,532,535,546,565,582,589,608,614,624,637,639,645,646,651
Seq#:5; N Pos. 655,657,660,661,673,682,688,692,701,716
Seq#:8; N Pos. 188,192,228,237,245,259,296,344,380,388,395,404,411,482,497
Seq#:8; N Pos. 590,640,657
Seq#:9; N Pos. 354,420,431,486,497,508,527,529,536,550,572,592,598,602,603
Seq#:9; N Pos. 610,619,621
Seq#:10; N Pos. 182,235,279,284,292,444,448,465,492,507,508,516,533,536,538
Seq#:10; N Pos. 544,551,562,565,573,576,577,579,581,583,593,595,602,604,608
Seq#:10; N Pos. 610,611,613,616,619,625,626
Seq#:13; Xaa Pos. 64,82,96,97,100,149,150,155,163,168,170,176,177,179,185
Seq#:13; Xaa Pos. 186,189,190,191,192,195,196,198,199,201,202,203,204,206
Seq#:16; Xaa Pos. 137,146,173,177,179,197,202,205,213

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Input Set : A:\5008.ST25.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:94 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:540
L:96 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:96 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:600
L:112 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:60
L:116 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:180
L:120 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:300
L:122 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:360
L:124 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:420
L:126 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:480
L:128 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:540
L:130 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:600
L:132 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:660
L:268 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:1
L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:2
L:272 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:300
L:274 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:360
L:278 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:420
L:280 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:480
L:282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:600
L:306 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:660
L:308 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:720
L:310 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:420
L:312 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:480
L:314 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:540
L:316 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9

VERIFICATION SUMMARY DATE: 04/23/2002
PATENT APPLICATION: US/09/555,981C TIME: 07:57:29

Input Set : A:\5008.ST25.txt
Output Set: N:\CRF3\04232002\I555981C.raw

L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:600
L:336 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:180
L:338 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:240
L:344 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:420
L:346 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:480
L:348 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:540
L:350 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:600
L:469 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:48
L:475 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:475 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:80
L:478 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:478 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:96
L:487 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:144
L:490 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:160
L:493 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:176
L:496 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:192
L:714 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:714 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:128
L:717 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:144
L:720 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:160
L:723 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:176
L:726 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:192
L:729 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:208